Clean Copy of Specification

Please replace the first full paragraph on page 11 with the following:

Figure 14 shows the amino acid sequence alignment of bacterial RT carried out according to Xiong and Eickbush EMBO Journal, 9(10): 3353-3362, (1990). Amino acids highly conserved in eukaryotic Rts are shown at the top of the sequences. These amino acids include largely unvaried residues or chemically similar residues. (h) Hydorphobic residue; (p) small polar residues; (c) charged residue. Amino acids conserved in all seven bacterial Rts (identical residues plus functional conserved residues indicated by h for hydrophobic residues or p for polar residues) are marked by solid dots at the bottom of the sequences. The consensus sequence shown at the bottom of the sequences is determined when five out of seven sequences contain an identical or chemically similar residue (h, hydrophobic residue; p, charged and polar residue). The subdomains 1 to 7 are according to Xiong and Eickbush (1990), which are boxed and indicated by numbers. The highly conserved YXDD sequences are also boxed. Numbers on the right indicate the amino acid positions from the amino terminus for each RT Sources for the sequences are Sal63 (Hsu et al. J. Bact., 174(7): 2384-2387, April 1992b) Seq. ID No. 34, Mx162 (Inouye et al. 1989) Seq. ID No. 33, Mx65 (Inouye et al. 1990) Seq. ID No. 32, Ec67 (Lampson et al. 1989b) Seq. ID No. 35, Ec86 (Lim and Maas 1989) Seq. ID No. 36, Ec73 (Sun, J., M. Inouye, and S. Inouye, 1991, Association of retroelement with a P4'-like cryptic prophage (retronphage ϕ R73) integrated into the selerocystyl tRNA gene of Escherichia coli. J. Bacteriol. 173:4171-4181.) Seq. ID No. 37, and Ec107 (Herzer, P.J., T. Kawaguchi, S. Inouye, and M.

Inouye. Direct integration of a retron (retron-Ec-107) into Escherichia coli genome by replacing a pallindromil 34-bb intergenic sequence. Mol. Microbiol., 1992.) Seq. ID No. 38.